



## RAW SEQUENCE LISTING ERROR REPORT

T3  
6300  
0889  
**BIOTECHNOLOGY  
SYSTEMS  
BRANCH**

TECH CENTER 1600/2900  
JUL 03 2001

RECEIVED

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/724,126

Source: OIPE

Date Processed by STIC: 12/7/2000

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)**

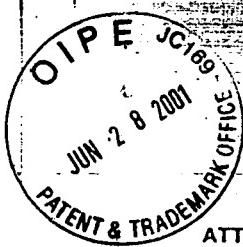
**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>**



# Raw Sequence Listing Error Summary

## ERROR DETECTED    SUGGESTED CORRECTION

SERIAL NUMBER:

09/724,126

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1  Wrapped Nucleic The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2  Wrapped Aminos The amino acid-number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3  Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4  Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5  Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6  Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7  PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8  Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9  Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:  
<210> sequence id number  
<400> sequence id number  
000
- 10  Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11  Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
- 12  Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13  PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

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OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/724,126DATE: 12/07/2000  
TIME: 07:57:43Input Set : A:\35966aseq.txt  
Output Set: N:\CRF3\12072000\I724126.rawDoes Not Comply  
Corrected Diskette Needed

4 <110> APPLICANT: Han, Hui-Quan  
5 Kwak, Keith  
7 <120> TITLE OF INVENTION: Human E3 Alpha Ubiquitin Ligase  
9 <130> FILE REFERENCE: 01017/35966  
OK 11 <140> CURRENT APPLICATION NUMBER: US/09/724,126  
12 <141> CURRENT FILING DATE: 2000-11-28  
14 <150> PRIOR APPLICATION NUMBER: US 60/187,911  
15 <151> PRIOR FILING DATE: 1999-03-08  
17 <160> NUMBER OF SEQ ID NOS: 29  
19 <170> SOFTWARE: PatentIn Ver. 2.0

## ERRORED SEQUENCES

508 <210> SEQ ID NO: 2  
509 <211> LENGTH: 1749  
510 <212> TYPE: PRT  
511 <213> ORGANISM: Homo sapiens  
513 <400> SEQUENCE: 2  
514 Met Ala Asp Glu Glu Ala Gly Gly Thr Glu Arg Met Glu Ile Ser Ala  
515 1 5 10 15  
516 Glu Leu Pro Gln Thr Pro Gln Arg Leu Ala Ser Trp Trp Asp Gln Gln  
517 20 25 30  
518 Val Asp Phe Tyr Thr Ala Phe Leu His His Leu Ala Gln Ieu Val Pro  
519 35 40 45  
520 Glu Ile Tyr Phe Ala Gln Met Asp Pro Asp Leu Glu Lys Gln Glu Glu  
521 50 55 60  
522 Ser Val Gln Met Ser Ile Phe Thr Pro Leu Glu Trp Tyr Leu Phe Gly  
523 65 70 75 80  
524 Glu Asp Pro Asp Ile Cys Leu Glu Lys Leu Lys His Ser Gly Ala Phe  
525 85 90 95  
526 Gin Leu Cys Gly Arg Val Phe Lys Ser Gly Glu Thr Thr Tyr Ser Cys  
527 100 105 110  
528 Arg Asp Cys Ala Ile Asp Pro Thr Cys Val Leu Cys Met Asp Cys Phe  
529 115 120 125  
530 Gln Asp Ser Val His Lys Asn His Arg Tyr Lys Met His Thr Ser Thr  
531 130 135 140  
532 Gly Gly Gly Phe Cys Asp Cys Gly Asp Thr Glu Ala Trp Lys Thr Gly  
533 145 150 155 160  
534 Pro Phe Cys Val Asn His Glu Pro Gly Arg Ala Gly Thr Ile Lys Glu  
535 165 170 175  
536 Asn Ser Arg Cys Pro Leu Asn Glu Glu Val Ile Val Gln Ala Arg Lys  
537 180 185 190  
538 Tle Phe Pro Ser Val Ile Lys Tyr Val Val Glu Met Thr Ile Trp Glu  
539 195 200 205  
540 Glu Glu Lys Glu Leu Pro Pro Gln Leu Gln Ile Arg Glu Lys Asn Glu  
541 210 215 220

pp45

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/724,126

DATE: 12/07/2000  
TIME: 07:57:43

Input Set : A:\35966aseq.txt  
Output Set: N:\CRF3\12072000\1724126.raw

556 Arg Tyr Tyr Cys Val Leu Phe Asn Asp Glu His His Ser Tyr Asp His  
 557 225 230 235 240  
 559 Val Ile Tyr Ser Leu Gin Arg Ala Leu Asp Cys Glu Leu Ala Glu Ala  
 560 245 250 255  
 562 Gin Leu His Thr Thr Ala Ile Asp Lys Glu Gly Arg Arg Ala Val Lys  
 563 260 265 270  
 565 Ala Gly Ala Tyr Ala Ala Cys Gin Glu Ala Lys Glu Asp Ile Lys Ser  
 566 275 280 285  
 568 His Ser Glu Asn Val Ser Cln His Pro Leu His Val Glu Val Leu His  
 569 290 295 300  
 571 Ser Glu Ile Met Ala His Gin Lys Phe Ala Leu Arg Leu Gly Ser Trp  
 572 305 310 315 320  
 574 Met Asn Lys Ile Met Ser Tyr Ser Ser Asp Phe Arg Gln Ile Phe Cys  
 575 325 330 335  
 577 Gln Ala Cys Leu Arg Glu Glu Pro Asp Ser Glu Asn Pro Cys Leu Ile  
 578 340 345 350  
 580 Ser Arg Leu Met Leu Trp Asp Ala Lys Leu Tyr Lys Gly Ala Arg Lys  
 581 355 360 365  
 583 Ile Leu His Glu Leu Ile Phe Ser Ser Phe Phe Met Glu Met Glu Tyr  
 584 370 375 380  
 586 Lys Lys Leu Phe Ala Met Glu Phe Val Lys Tyr Tyr Lys Gln Leu Gln  
 587 385 390 395 400  
 589 Lys Glu Tyr Ile Ser Asp Asp His Asp Arg Ser Ile Ser Ile Thr Ala  
 590 405 410 415  
 592 Leu Ser Val Gin Met Phe Thr Val Pro Thr Leu Ala Arg His Leu Ile  
 593 420 425 430  
 595 Glu Glu Gln Asn Val Ile Ser Val Ile Thr Glu Thr Leu Leu Glu Val  
 596 435 440 445  
 598 Leu Pro Glu Tyr Leu Asp Arg Asn Asn Lys Phe Asn Phe Gln Gly Tyr  
 599 450 455 460  
 601 Ser Gln Asp Lys Leu Gly Arg Val Tyr Ala Val Ile Cys Asp Leu Lys  
 602 465 470 475 480  
 604 Tyr Ile Leu Ile Ser Lys Pro Thr Ile Trp Thr Glu Arg Leu Arg Met  
 605 485 490 495  
 607 Gln Phe Leu Glu Gly Phe Arg Ser Phe Leu Lys Ile Leu Thr Cys Met  
 608 500 505 510  
 610 Gln Gly Met Glu Glu Ile Arg Arg Gln Val GLY Gln His Ile Glu Val  
 611 515 520 525  
 613 Asp Pro Asp Itp Glu Ala Ala Ile Ala Ile Gln Met Gln Leu Lys Asn  
 614 530 535 540  
 616 Ile Leu Leu Met Phe Gin Glu Trp Cys Ala Cys Asp Glu Glu Leu Leu  
 617 545 550 555 560  
 619 Leu Val Ala Tyr Lys Glu Cys His Lys Ala Val Met Arg Cys Ser Thr  
 620 565 570 575  
 622 Ser Phe Ile Ser Ser Ser Lys Thr Val Val Gln Ser Cys Gly His Ser  
 623 580 585 590  
 625 Leu Glu Thr Lys Ser Tyr Arg Val Ser Glu Asp Leu Val Ser Ile His  
 626 595 600 605  
 628 Leu Pro Leu Ser Arg Thr Leu Ala Gly Leu His Val Arg Leu Ser Arg

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/724,126

DATE: 12/07/2000  
 TIME: 07:57:43

Input Set : A:\35966aseq.txt  
 Output Set: N:\CRF3\12072000\I724126.raw

629	610	615	620														
631	Ieu	Gly	Ala	Val	Ser	Arg	Leu	His	Glu	Phe	Vai	Ser	Phe	Glu	Asp	Phe	
632	625						630		635								640
634	Gln	Val	Glu	Val	Ieu	Val	Glu	Tyr	Pro	Leu	Arg	Cys	Ieu	Val	Ieu	Val	
635										650							655
637	Ala	Gln	Val	Val	Ala	Gln	Met	Irp	Arg	Arg	Asn	Gly	Leu	Ser	Leu	Ile	
638										665							670
640	Ser	Gln	Val		Phe	Tyr	Tyr	Gln	Asp	Vai	Lys	Cys	Arg	Glu	Glu	Met	Tyr
641										680							685
643	Asp	Lys	Asp	Ile	Ile	Met	Leu	Gln	Ile	Gly	Ala	Ser	Leu	Met	Asp	Pro	
644										695							700
646	Asn	Lys	Phe	Ieu	Leu	Leu	Val	Ieu	Glu	Arg	Tyr	Glu	Ieu	Ala	Gln	Ala	
647										710							720
649	Phe	Asn	Lys	Thr	Ile	Ser	Ihr	Lys	Asp	Gln	Asp	Leu	Ile	Lys	Gln	Tyr	
650										725							735
652	Asn	Ihr	Leu	Ile	Glu	Glu	Met	Leu	Gln	Val	Leu	Ile	Tyr	Ile	Val	Gly	
653										740							750
655	Glu	Arg	Tyr	Vai	Pro	Gly	Vai	Gly	Asn	Vai	Tnr	Lys	Glu	Glu	Val	Ihr	
656										755							765
658	Met	Arg	Glu	Ile	Ile	His	Leu	Leu	Cys	Ile	Glu	Pro	Met	Pro	His	Ser	
659										770							780
661	Ala	Ile	Ala	Lys	Asn	Leu	Pro	Glu	Asn	Glu	Asn	Asn	Glu	Thr	Gly	Leu	
662										785							800
664	Glu	Asn	Val	Ile	Asn	Lys	Val	Ala	Thr	Phe	Lys	Lys	Pro	Gly	Vai	Ser	
665										805							815
667	Gly	His	Gly	Val	Tyr	Glu	Leu	Lys	Asp	Glu	Ser	Leu	Lys	Asp	Phe	Asn	
668										820							830
670	Met	Tyr	Phe	Tyr	His	Tyr	Ser	Lys	Thr	Gln	His	Ser	Lys	Ala	Glu	His	
671										835							845
673	Met	Gln	Lys	Lys	Arg	Arg	Lys	Gln	Glu	Asn	Lys	Asp	Gln	Ala	Leu	Pro	
674										850							860
676	Pro	Pro	Pro	Pro	Glu	Phe	Cys	Pro	Ala	Phe	Ser	Lys	Vai	Ile	Asn		
677										870							880
679	Leu	Leu	Asn	Cys	Asp	Ile	Met	Met	Tyr	Ile	Leu	Arg	Ihr	Vai	Phe	Gln	
680										885							895
682	Arg	Ala	Ile	Asp	Thr	Asp	Ser	Asn	Leu	Irp	Thr	Glu	Gly	Met	Leu	Gln	
683										900							910
685	Met	Ala	Phe	His	Ile	Leu	Ala	Leu	Gly	Leu	Leu	Glu	Lys	Gln	Gln		
686										915							925
688	Leu	Gln	Lys	Ala	Pro	Glu	Glu	Glu	Vai	Ihr	Phe	Asp	Phe	Tyr	His	Lys	
689										930							940
691	Ala	Ser	Arg	Leu	Gly	Ser	Ser	Ala	Met	Asn	Ile	Gln	Met	Leu	Leu	Gln	
692										945							955
694	Lys	Leu	Lys	Gly	Ile	Pro	Gln	Leu	Gly	Gly	Gln	Lys	Asp	Met	Ile	Thr	
695										955							975
697	Irp	Ile	Leu	Gln	Met	Phe	Asp	Thr	Vai	Lys	Arg	Leu	Arg	Glu	Lys	Ser	
698										965							990
700	Cys	Leu	Ile	Val	Ala	Thr	Thr	Ser	Gly	Ser	Glu	Ser	Ile	Lys	Asn	Asp	
701										995							1005